

0430

JHDO



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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/043,787

DATE: 02/11/2002

TIME: 10:01:45

Input Set : F:\46699-20002.txt

Output Set: N:\CRF3\02112002\J043787.raw

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# 2

4 <110> APPLICANT: Yuan, Chong-Sheng  
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING  
 7 HOMOCYSTEINE  
 9 <130> FILE REFERENCE: 46699-20002.21  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/043,787  
 C--> 12 <141> CURRENT FILING DATE: 2002-01-10  
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 15 <151> PRIOR FILING DATE: 2001-06-29  
 17 <150> PRIOR APPLICATION NUMBER: US 09/457,205  
 18 <151> PRIOR FILING DATE: 1999-12-06  
 20 <150> PRIOR APPLICATION NUMBER: US 09/347,878  
 21 <151> PRIOR FILING DATE: 1999-07-06  
 23 <160> NUMBER OF SEQ ID NOS: 184  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 28 <211> LENGTH: 432  
 29 <212> TYPE: PRT  
 30 <213> ORGANISM: Homo sapiens  
 32 <400> SEQUENCE: 1  
 33 Met Ser Asp Lys Leu Pro Tyr Lys Val Ala Asp Ile Gly Leu Ala Ala  
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 35 Trp Gly Arg Lys Ala Leu Asp Ile Ala Glu Asn Glu Met Pro Gly Leu  
 36 20 25 30  
 37 Met Arg Met Arg Glu Arg Tyr Ser Ala Ser Lys Pro Leu Lys Gly Ala  
 38 35 40 45  
 39 Arg Ile Ala Gly Cys Leu His Met Thr Val Glu Thr Ala Val Leu Ile  
 40 50 55 60  
 41 Glu Thr Leu Val Thr Leu Gly Ala Glu Val Gln Trp Ser Ser Cys Asn  
 42 65 70 75 80  
 43 Ile Phe Ser Thr Gln Asn His Ala Ala Ala Ile Ala Lys Ala Gly  
 44 85 90 95  
 45 Ile Pro Val Tyr Ala Trp Lys Gly Glu Thr Asp Glu Glu Tyr Leu Trp  
 46 100 105 110  
 47 Cys Ile Glu Gln Thr Leu Tyr Phe Lys Asp Gly Pro Leu Asn Met Ile  
 48 115 120 125  
 49 Leu Asp Asp Gly Gly Asp Leu Thr Asn Leu Ile His Thr Lys Tyr Pro  
 50 130 135 140  
 51 Gln Leu Leu Pro Gly Ile Arg Gly Ile Ser Glu Glu Thr Thr Thr Gly  
 52 145 150 155 160  
 53 Val His Asn Leu Tyr Lys Met Met Ala Asn Gly Ile Leu Lys Val Pro  
 54 165 170 175  
 55 Ala Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn Leu  
 56 180 185 190

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57 Tyr Gly Cys Arg Glu Ser Leu Ile Asp Gly Ile Lys Arg Ala Thr Asp
58           195                200                205
59 Val Met Ile Ala Gly Lys Val Ala Val Val Ala Gly Tyr Gly Asp Val
60       210                215                220
61 Gly Lys Gly Cys Ala Gln Ala Leu Arg Gly Phe Gly Ala Arg Val Ile
62 225                230                235                240
63 Ile Thr Glu Ile Asp Pro Ile Asn Ala Leu Gln Ala Ala Met Glu Gly
64           245                250                255
65 Tyr Glu Val Thr Thr Met Asp Glu Ala Cys Gln Glu Gly Asn Ile Phe
66           260                265                270
67 Val Thr Thr Thr Gly Cys Ile Asp Ile Ile Leu Gly Arg His Phe Glu
68           275                280                285
69 Gln Met Lys Asp Asp Ala Ile Val Cys Asn Ile Gly His Phe Asp Val
70       290                295                300
71 Glu Ile Asp Val Lys Trp Leu Asn Glu Asn Ala Val Glu Lys Val Asn
72 305                310                315                320
73 Ile Lys Pro Gln Val Asp Arg Tyr Arg Leu Lys Asn Gly Arg Arg Ile
74           325                330                335
75 Ile Leu Leu Ala Glu Gly Arg Leu Val Asn Leu Gly Cys Ala Met Gly
76           340                345                350
77 His Pro Ser Phe Val Met Ser Asn Ser Phe Thr Asn Gln Val Met Ala
78           355                360                365
79 Gln Ile Glu Leu Trp Thr His Pro Asp Lys Tyr Pro Val Gly Val His
80       370                375                380
81 Phe Leu Pro Lys Lys Leu Asp Glu Ala Val Ala Glu Ala His Leu Gly
82 385                390                395                400
83 Lys Leu Asn Val Lys Leu Thr Lys Leu Thr Glu Lys Gln Ala Gln Tyr
84           405                410                415
85 Leu Gly Met Ser Cys Asp Gly Pro Phe Lys Pro Asp His Tyr Arg Tyr
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88 &lt;210&gt; SEQ ID NO: 2

89 &lt;211&gt; LENGTH: 2211

90 &lt;212&gt; TYPE: DNA

91 &lt;213&gt; ORGANISM: Homo sapiens

93 &lt;400&gt; SEQUENCE: 2

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95 tgccctacaa agtcgccgac atcggcctgg ctgcctgggg acgcaaggcc ctggacattg      120
96 ctgagaacga gatgccgggc ctgatgcgta tgcgggagcg gtactcggcc tccaagccac      180
97 tgaagggcgc ccgcatcgct ggtgcctgc acatgaccgt ggagacggcc gtccctcattg      240
98 agaccctcgt caccctgggt gctgaggtgc agtgggtccag ctgcaacatc ttctccaccc      300
99 agaaccatgc ggcggctgcc attgccaagg ctggcattcc ggtgtatgcc tggaagggcg      360
100 aaacggacga ggagtacctg tggatgattg agcagaccct gtacttcaag gacgggcccc      420
101 tcaacatgat tctggacgac gggggcgacc tcaccaacct catccacacc aagtaccgcg      480
102 agcttctgcc aggcattccga ggcattctctg aggagaccac gactggggtc cacaacctct      540
103 acaagatgat ggccaatggg atcctcaagg tgcctgccat caatgtcaat gactccgtca      600
104 ccaagagcaa gtttgacaac ctctatggct gccgggagtc cctcatagat ggcattcaagc      660
105 gggccacaga tgtgatgatt gccggcaagg tagcgggtgg agcaggctat ggtgatgtgg      720
106 gcaagggctg tgcccaggcc ctgcgggggt tcggagcccg cgtcatcatc accgagattg      780
107 accccatcaa cgcactgcag gctgccatgg agggctatga ggtgaccacc atggatgagg      840

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108 cctgtcagga gggcaacatc tttgtcacca ccacaggctg tattgacatc atccttggcc 900
109 ggtaggtgcc agatgggggg tcccggggag tgagggagga gggcagagtt gggacagctt 960
110 tctgtcccctg acaatctccc acggtcttgg gctgcctgac aggcactttg agcagatgaa 1020
111 ggatgatgcc atttgtgtga acattggaca ctttgacgtg gagatcgatg tcaagtggct 1080
112 caacgagaac gccgtggaga aggtgaacat caagccgcag gtggaccggg atcggttgaa 1140
113 gaatgggcgc cgcacatcc tgctggccga gggtcggctg gtcaacctgg gttgtgccat 1200
114 gggccacccc agcttcgtga tgagtaactc cttcaccaac caggtgatgg cgcagatcga 1260
115 gctgtggacc catccagaca agtaccctgt tggggttcat ttcctgcccagaagctgga 1320
116 tgaggcagtg gctgaagccc acctgggcaa gctgaatgtg aagttgacca agctaactga 1380
117 gaagcaagcc cagtacctgg gcatgtcctg tgatggcccc ttcaagccgg atcactaccg 1440
118 ctactgagag ccaggtctgc gtttcacctt ccagctgctg tccttgcccaggccccacct 1500
119 ctctccccta agagctaata gccaacactt tgtgattggt ttgtcagtgt ccccatcga 1560
120 ctctctgggg ctgatcactt agtttttggc ctctgctgca gccgtcatac tgttccaaat 1620
121 gtggcagcgg gaacagagta ccctcttcaa gccccgttca tgatggaggt cccagccaca 1680
122 gggaaacctg agctcagtg tcttggaaaca gctcactaag tcagtccttc cttagcctgg 1740
123 aagtcagtag tggagtcaca aagcccatgt gttttgccat ctaggccttc acctggtctg 1800
124 tggacttata cctgtgtgct tggtttacag gtccagtggt tcttcagccc atgacagatg 1860
125 agaaggggct atattgaagg gcaaagagga actgttgttt gaattttcct gagagcctgg 1920
126 cttagtgctg ggccttctct taaacctcat tacaatgagg ttagtacttt tagtccctgt 1980
127 ttacagggg ttagaataga ctgttaagg gcaactgaga aagaacagag aagtgcagc 2040
128 taggggttga gaggggccag aaaaacatga atgcaggcag atttcgtgaa atctgccacc 2100
129 actttataac cagatggttc ctttcacaac cctgggtcaa aaagagaata atttggccta 2160
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135 <213> ORGANISM: Homo sapiens
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138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: (1)...(2226)
140 <223> OTHER INFORMATION: n = A,T,C or G
142 <400> SEQUENCE: 3
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145 tggaccatac taccaaggac cagtccacct gaaccacaca ctctaaagaa atatttttta 180
146 agataacttt tattttcttc ttaactcctt cctcttgatt tttttcctat aatttcattc 240
147 ttgttttttc atctcattat ccaagttctg cagaccacac aggaacttgc ttcattggctc 300
148 tttagatgaa atagaagttc agggttcctc actctagtca ctaaagaagg attttactct 360
149 cccagcccag aaaggtgatt ctttctttac catttctggg gacttttagtc ttaattaggt 420
150 accttattaa caggaaatgc taaggtacct tctctgtgga acaatctgca atgtctaaat 480
151 cgccttaaaa gagcccattt cttagctgct gaaatcagtg ctctttcact tcttcagaga 540
152 agcagggatg gtacctaccc ggcaggtagg ttagatgtgg gtggtgcatg ttaatttccc 600
153 ttagaagttc caagccctgt ttcctgcgta aaggtggtat gtccagttca gagatgtgta 660
154 taatgagcat ggcttggtta gatcaggagg cccacttgga tttatagtat agcccttccct 720
155 ccactcccac cagacttgcct catttttcga gtttttaact agactacact ctattgagtt 780
W--> 156 taattttgtc ctctaggatt tattttctgt gtccaaaaaa aaaaanaaaag aaaagaaaaa 840
157 ttaaggagaa tttttggtgt taatgctgag gaattgcttg agtggttagt tgttaccaat 900
158 ttctcttttg aacctttgga gctaaggatg ctgagtctag agaaatgcta gtctcaagcc 960
159 ctgttaagtc cctctgtttc tagcccgtag ttcatagcat cagtgaactg gagccacaac 1020

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160 agcaaattct atcagctgtg taccatacag cttgtgctga aggcgaattt cttgagccat 1080
161 tactcagtat aaagcactga gttctatctt taggatttat ctttaagagc aaatttctgg 1140
162 tcagctgtgc ttctgcaacc taaaatattt aaagggaggt aggtgtgggc aggaggagga 1200
163 atgataaatt gggccagggc aagaaaaatc tagcttcata taatttgtct gggactatac 1260
164 accctatata atgttagttt tacagaagta atatgacttt tgattgctac ataccacaaa 1320
165 gagtttatga actgagatca taaagggcaa ctgatgtgtg aagaaagtag tcagtacatc 1380
166 ctggctcatg ctctgaaaga atatccagag aggcctcttc aaagatcagg gagatgtatt 1440
167 cccatgccat gcaccctgct tcccagcatt tctgcatggg caagtgaagt ttatgctcat 1500
168 gagctttaag tatataatta tccaggattt taaatcctca acttggttcta gcttgtgatc 1560
169 cctcaaagtt gggtcatacg ttagtgctag atactagaaa ttttcacttt tccactgatc 1620
170 agagagacag acattaaaaa caaaaataga agaaaggaaa gctttcaccc tgcagcttct 1680
171 tagcagggaa caattgtctt gccaaaactt ttttcccttt tctctcccat tttcttttac 1740
172 ccaatccctt cttactcctt gccagtgtga ccatgctttc ttctctgtag atgttaacag 1800
173 ttaaggccta ttttccctcg gcacttaacc aaccaatcag aacaccacat ctgttagggg 1860
174 aggtaacctg gccaacagtg tatccatcac gtttagccctg ctggagggaa gggaccacaa 1920
175 ttcacctgcc ctctgacctg ccccttgatc ccatatctat taccgtgtcc ataggaataa 1980
176 taggtaaggg ctctgtctct gtcaagccat gtaacaaagg acactgttaa aaaaaaaaaa 2040
177 aagtctggca tcagaggagg catgtggaga gcaactggg aagaacaagt tcattttgta 2100
178 ttgaatgatt ttaaatgaat gcaatattaa tccttgaga tgagcaataa tcattaaaat 2160
W--> 179 cgattaaaaat grtaagrcct taaaaaaaaa aaanaaggmn gagaaggang gnnnggggtg 2220
W--> 180 nngngg 2226
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183 <211> LENGTH: 27
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Primer
190 <400> SEQUENCE: 4
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194 <211> LENGTH: 27
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
200 of human SAH hydrolases
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203 gacttcgtca ccgccagcaa gtttggg 27
205 <210> SEQ ID NO: 6
206 <211> LENGTH: 27
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208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
212 of human SAH hydrolases
214 <400> SEQUENCE: 6
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219 <212> TYPE: DNA
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222 <220> FEATURE:
223 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
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226 <400> SEQUENCE: 7
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229 <210> SEQ ID NO: 8
230 <211> LENGTH: 27
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232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
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238 <400> SEQUENCE: 8
239 gatctccacg tcagagtgtc caatgtt
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243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
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250 <400> SEQUENCE: 9
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253 <210> SEQ ID NO: 10
254 <211> LENGTH: 27
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
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262 <400> SEQUENCE: 10
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265 <210> SEQ ID NO: 11
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268 <213> ORGANISM: Artificial Sequence
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271 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
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274 <400> SEQUENCE: 11
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277 <210> SEQ ID NO: 12
278 <211> LENGTH: 27
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/043,787

DATE: 02/11/2002

TIME: 10:01:46

Input Set : F:\46699-20002.txt

Output Set: N:\CRF3\02112002\J043787.raw

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
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L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:472 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28